UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/530,219	07/27/2000	Christof Niehrs	40168	4031

7590   11/28/2001

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Berdo & Goodman
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1300 19th Street
Washington, DC   20036

EXAMINER
ANDRES, JANET L

ART UNIT	PAPER NUMBER
1646	

DATE MAILED: 11/28/2001

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 07-01)

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/530219	07/27/00	Niehrs	40168

EXAMINER	
Janet Andres	
ART UNIT	PAPER NUMBER
1646	9

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.R.F. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Janet Andres whose telephone number is (703) 305-0557. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Yvonne Eyler whose telephone number is (703) 308-6564. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

YVONNE EYLER, PH.D
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

[ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

[ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

[X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

[ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

[ ] 7. Other:
Applicant Must Provide:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

[X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
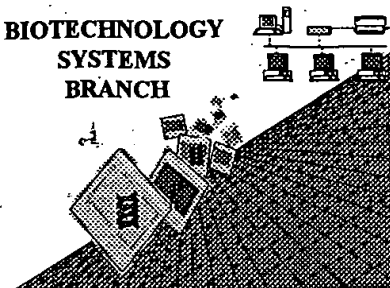For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
    Technical Assistance.......................................703-287-0200
    To Purchase PatentIn Software........................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: *09/530,219A*

Source: *OIPE*

Date Processed by STIC: *9/20/2001*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE**
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A**
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u>
<u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/530,2194

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) ___ 8 ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 09/20/2001
PATENT APPLICATION: US/09/530,219A   TIME: 10:43:27

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  4        GLINKA, ANDREI
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 11 <141> CURRENT FILING DATE: 2001-09-10
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192 tcctttgtac agcagaaata aacgtatcag tactcgtact cattaaaaaa acacacggag 1380
193 cat                                                                  1383
196 <210> SEQ ID NO: 8
197 <211> LENGTH: 44
198 <212> TYPE: PRT
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus wnt
203       Protein
205 <220> FEATURE:
206 <221> NAME/KEY: MOD_RES
207 <222> LOCATION: (2)..(8)
208 <223> OTHER INFORMATION: Any Amino Acid
210 <220> FEATURE:
211 <221> NAME/KEY: MOD_RES
212 <222> LOCATION: (9)
213 <223> OTHER INFORMATION: More Than One Amino Acid
215 <220> FEATURE:
216 <221> NAME/KEY: MOD_RES
217 <222> LOCATION: (10)..(16)
218 <223> OTHER INFORMATION: Any Amino Acid
220 <220> FEATURE:
221 <221> NAME/KEY: MOD_RES
222 <222> LOCATION: (18)..(19)
223 <223> OTHER INFORMATION: Any Amino Acid
225 <220> FEATURE:
226 <221> NAME/KEY: MOD_RES
227 <222> LOCATION: (21)..(26)
228 <223> OTHER INFORMATION: Any Amino Acid
230 <220> FEATURE:
231 <221> NAME/KEY: MOD_RES
232 <222> LOCATION: (28)..(32)
```

invalid - see item 5 on Error Summary Sheet (handwritten annotation)

```
     233 <223> OTHER INFORMATION: Any Amino Acid
     235 <220> FEATURE:
     236 <221> NAME/KEY: MOD_RES
     237 <222> LOCATION: (35)..(38)
     238 <223> OTHER INFORMATION: Any Amino Acid
     240 <220> FEATURE:
     241 <221> NAME/KEY: MOD_RES
     242 <222> LOCATION: (40)..(41)
     243 <223> OTHER INFORMATION: Any Amino Acid
     245 <220> FEATURE:
     246 <221> NAME/KEY: MOD_RES
     247 <222> LOCATION: (43)
     248 <223> OTHER INFORMATION: Any Amino Acid
     250 <400> SEQUENCE: 8
W--> 251 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     252   1               5                  10                  15
W--> 254 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
     255          20                  25                  30
W--> 257 Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Gly Xaa Cys
     258          35                  40
     261 <210> SEQ ID NO: 9
     262 <211> LENGTH: 65
     263 <212> TYPE: PRT
     264 <213> ORGANISM: Artificial Sequence
     266 <220> FEATURE:
     267 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus wnt
     268       Protein
     270 <220> FEATURE:
     271 <221> NAME/KEY: MOD_RES
     272 <222> LOCATION: (2)..(3)
     273 <223> OTHER INFORMATION: Any Amino Acid
     275 <220> FEATURE:
     276 <221> NAME/KEY: MOD_RES
     277 <222> LOCATION: (5)..(6)
     278 <223> OTHER INFORMATION: Any Amino Acid
     280 <220> FEATURE:
     281 <221> NAME/KEY: MOD_RES
     282 <222> LOCATION: (8)..(11)
     283 <223> OTHER INFORMATION: Any Amino Acid
     285 <220> FEATURE:
     286 <221> NAME/KEY: MOD_RES
     287 <222> LOCATION: (14)..(15)
     288 <223> OTHER INFORMATION: Any Amino Acid
     290 <220> FEATURE:
     291 <221> NAME/KEY: MOD_RES
     292 <222> LOCATION: (17)
     293 <223> OTHER INFORMATION: Any Amino Acid
     295 <220> FEATURE:
     296 <221> NAME/KEY: MOD_RES
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 09/20/2001
PATENT APPLICATION: US/09/530,219A   TIME: 10:43:28

Input Set : **A:\40168.app**
Output Set: **N:\CRF3\09202001\I530219A.raw**

```
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
```